

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 08/439,095  
Source: JFW/6  
Date Processed by STIC: 03/13/2006

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 03/13/2006

PATENT APPLICATION: US/08/439,095

TIME: 14:53:53

Input Set : A:\ 140140279US.SEQLIST.TXT

Output Set: N:\CRF4\03132006\H439095.raw

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4 <110> APPLICANT: Matsui, Toshimitsu
5      Aaronson, Stuart H.
6      Pierce, Jacalyn H.
8 <120> TITLE OF INVENTION: TYPE ALPHA PLATELET DERIVED GROWTH
9      FACTOR RECEPTOR
11 <130> FILE REFERENCE: 14014.0279US
13 <140> CURRENT APPLICATION NUMBER: 08/439,095
14 <141> CURRENT FILING DATE: 1995-05-11
16 <150> PRIOR APPLICATION NUMBER: 07/915,884
17 <151> PRIOR FILING DATE: 1992-07-20
18 <150> PRIOR APPLICATION NUMBER: 07/308,282
19 <151> PRIOR FILING DATE: 1989-02-09
22 <160> NUMBER OF SEQ ID NOS: 2
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1089
28 <212> TYPE: PRT
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
33      Synthetic Construct
35 <400> SEQUENCE: 1
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37 1          5          10          15
38 Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile Leu Pro
39          20          25          30
40 Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg
41          35          40          45
42 Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu
43          50          55          60
44 Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser Gly Leu
45 65          70          75          80
46 Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly
47          85          90          95
48 Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu
49          100         105         110
50 Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe
51          115         120         125
52 Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp
53          130         135         140
54 Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr
55 145         150         155         160
56 Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln

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57          165          170          175
58 Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr
59          180          185          190
60 Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu
61          195          200          205
62 Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val
63          210          215          220
64 Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn
65 225          230          235          240
66 Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys
67          245          250          255
68 Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val
69          260          265          270
70 Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr
71          275          280          285
72 Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys
73          290          295          300
74 Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr
75 305          310          315          320
76 Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val
77          325          330          335
78 Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn
79          340          345          350
80 Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu
81          355          360          365
82 Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala
83          370          375          380
84 Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp
85 385          390          395          400
86 Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser
87          405          410          415
88 Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr
89          420          425          430
90 Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met
91          435          440          445
92 Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile
93          450          455          460
94 Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp
95 465          470          475          480
96 Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr
97          485          490          495
98 Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg
99          500          505          510
100 Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala
101          515          520          525
102 Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val
103          530          535          540
104 Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg
105 545          550          555          560

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106 Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp
107          565          570          575
108 Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly
109          580          585          590
110 Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val
111          595          600          605
112 Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val
113          610          615          620
114 Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala
115 625          630          635          640
116 Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn
117          645          650          655
118 Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile
119          660          665          670
120 Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys
121          675          680          685
122 Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu
123 690          695          700
124 Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr
125 705          710          715          720
126 Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln
127          725          730          735
128 Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser
129          740          745          750
130 Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr
131          755          760          765
132 Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp
133          770          775          780
134 Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe Thr Tyr
135 785          790          795          800
136 Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His
137          805          810          815
138 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val
139          820          825          830
140 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn
141          835          840          845
142 Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro
143          850          855          860
144 Glu Ser Ile Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser
145 865          870          875          880
146 Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr
147          885          890          895
148 Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly
149          900          905          910
150 Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile
151          915          920          925
152 Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr
153          930          935          940
154 His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys

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155 945          950          955          960
156 Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala
157          965          970          975
158 Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr
159          980          985          990
160 Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp
161          995          1000          1005
162 Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp
163          1010          1015          1020
164 Ile Asp Pro Val Pro Glu Glu Glu Asp Leu Gly Lys Arg Asn Arg His
165 1025          1030          1035          1040
166 Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser
167          1045          1050          1055
168 Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met
169          1060          1065          1070
170 Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe
171          1075          1080          1085
172 Leu
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 6413
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
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182     Synthetic Construct
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187 gagaagtttc ccagagctat ggggacttcc catccggcgt tcctggtctt aggtgtctt      180
188 ctcacagggc tgagcctaat cctctgccag ctttcattac cctctatcct tccaaatgaa      240
189 aatgaaaagg ttgtgcagct gaattcatcc ttttctctga gatgcttttg ggagagttaa      300
190 gtgagctggc agtaccatcat gtctgaagaa gagagctccg atgtggaaat cagaaatgaa      360
191 gaaaacaaca gcggcctttt tgtgacggtc ttggaagtga gcagtgcctc ggcggccac      420
192 acagggttgt acacttgcta ttacaaccac actcagacag aagagaatga gcttgaaggc      480
193 aggcacattht acatctatgt gccagaccca gatgtagcct ttgtacctct aggaatgacg      540
194 gattattttag tcatcgtgga ggatgatgat tctgccatta taccttgctc cacaactgat      600
195 cccgagactc ctgtaacctt acacaacagt gagggggttg tacctgcctc ctacgacagc      660
196 agacagggct ttaatgggac cttcactgta gggccctata tctgtgaggc caccgtcaaa      720
197 ggaaagaagt tccagaccat cccatttaat gtttatgctt taaaagcaac atcagagctg      780
198 gatctagaaa tggaaagctct taaaaccgtg tataagtcag gggaaacgat tgtggtcacc      840
199 tgtgctgttt ttaacaatga ggtggttgac cttcaatgga cttaccctgg agaagtgaaa      900
200 ggcaaaggca tcacaatgct ggaagaaatc aaagtcccat ccatcaaatt ggtgtacact      960
201 ttgacgggtc ccgaggccac ggtgaaagac agtggagatt acgaatgtgc tgcccgccag      1020
202 gctaccaggg aggtcaaaaga aatgaagaaa gtcactattht ctgtccatga gaaaggtttc      1080
203 attgaaatca aacccacctt cagccagttg gaagctgtca acctgcatga agtcaaacat      1140
204 tttgtttag aggtgcgggc ctacccacct cccaggatat cctggctgaa aaacaatctg      1200
205 actctgattg aaaatctcac tgagatcacc actgatgtgg aaaagattca ggaaataagg      1260
206 tatcgaagca aattaaagct gatccgtgct aaggaagaag acagtggcca ttatactatt      1320
207 gtagctcaaa atgaagatgc tgtgaagagc tatacttttg aactgttaac tcaagtctct      1380

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|     |             |             |             |             |             |             |      |
|-----|-------------|-------------|-------------|-------------|-------------|-------------|------|
| 208 | tcatccattc  | tggacttggg  | cgatgatcac  | catgggtcaa  | ctgggggaca  | gacggtgagg  | 1440 |
| 209 | tgcacagctg  | aaggcacgcc  | gcttcctgat  | attgagtggg  | tgatatgcaa  | agatattaag  | 1500 |
| 210 | aaatgtaata  | atgaaacttc  | ctggactatt  | ttggccaaca  | atgtctcaaa  | catcatcacg  | 1560 |
| 211 | gagatccact  | cccagagacg  | gagtaccgtg  | gagggccgtg  | tgactttcgc  | caaagtggag  | 1620 |
| 212 | gagaccatcg  | ccgtgcgatg  | cctggctaag  | aatctccttg  | gagctgagaa  | ccgagagctg  | 1680 |
| 213 | aagctggtgg  | ctcccaccct  | gcgttctgaa  | ctcacggtgg  | ctgctgcagt  | cctggtgctg  | 1740 |
| 214 | ttggtgattg  | tgatcatctc  | acttattgtc  | ctggttgtca  | tttgaaaca   | gaaaccgagg  | 1800 |
| 215 | tatgaaattc  | gctggagggt  | cattgaatca  | atcagcccgg  | atggacatga  | atatatttat  | 1860 |
| 216 | gtggacccga  | tgacagctgcc | ttatgactca  | agatgggagt  | ttccaagaga  | tggactagt   | 1920 |
| 217 | cttggtcggg  | tcttgggggtc | tggagcggtt  | gggaagggtg  | ttgaaggaaac | agcctatgga  | 1980 |
| 218 | ttaagccggg  | cccaacctgt  | catgaaagtt  | gcagtgaaga  | tgctaaaacc  | cacggccaga  | 2040 |
| 219 | tccagtga    | aaacagctct  | catgtctgaa  | ctgaagataa  | tgactcacct  | ggggccacat  | 2100 |
| 220 | ttgaacattg  | taaacttgct  | gggagcctgc  | accaagtcag  | gccccattta  | catcatcaca  | 2160 |
| 221 | gagtattgct  | tctatggaga  | tttggtaaac  | tatttgcata  | agaataggga  | tagcttctctg | 2220 |
| 222 | agccaccacc  | cagagaagcc  | aaagaaaagc  | ctggatatct  | ttggattgaa  | ccctgctgat  | 2280 |
| 223 | gaaagcacac  | ggagctatgt  | tattttatct  | tttgaaaaca  | atggtgacta  | catggacatg  | 2340 |
| 224 | aagcaggctg  | atactacaca  | gtatgtcccc  | atgctagaaa  | ggaaaagagg  | ttctaaatat  | 2400 |
| 225 | tccgacatcc  | agagatcact  | ctatgatcgt  | ccagcctcat  | ataagaagaa  | atctatgtta  | 2460 |
| 226 | gactcagaag  | tcaaaaacct  | gcttcctgat  | gataagtcag  | aaggccttac  | tttattggat  | 2520 |
| 227 | ctgttgagct  | tcaacctatca | agctgcctga  | ggaatggagc  | ctttggtctc  | aaaaaaatgt  | 2580 |
| 228 | gtccaccgtg  | atctggctgc  | tgcgaacgtc  | ctcctggcac  | aaggaaaaat  | tgtgaagatc  | 2640 |
| 229 | tgtgactttg  | gcctggccag  | agacatcatg  | catgattcga  | actatgtgtc  | gaaaggcagt  | 2700 |
| 230 | acctttctgc  | ccgtgaagtg  | gatggctcct  | gagagcatct  | ttgacaacct  | ctacaccaca  | 2760 |
| 231 | ctgagtgatg  | tctggtctta  | tggcattctg  | ctctgggaga  | tcttttccct  | tgggtggacc  | 2820 |
| 232 | ccttaccctg  | gcatgatggg  | ggattctact  | ttctacaata  | agatcaagag  | tgggtaccgg  | 2880 |
| 233 | atggccaagc  | ctgaccacgc  | taccagtga   | gtctacgaga  | tcatggtgaa  | atgctggaac  | 2940 |
| 234 | agtgagccgg  | agaagagacc  | ctccttttac  | cacctgagt   | agattgtgga  | gaatctgctg  | 3000 |
| 235 | cctggacaat  | ataaaaagag  | ttatgaaaaa  | attcacctgg  | acttcctgaa  | gagtgaccat  | 3060 |
| 236 | cctgctgtgg  | cacgcatg    | tgtggactca  | gacaatgcat  | acattgggtg  | cacctacaaa  | 3120 |
| 237 | aacgaggaag  | acaagctgaa  | ggactgggag  | ggtggtctgg  | atgagcagag  | actgagcgtg  | 3180 |
| 238 | gacagtggct  | acatcattcc  | tctgcctgac  | attgaccctg  | tccctgagga  | ggaggacctg  | 3240 |
| 239 | ggcaagagga  | acagacacag  | ctcgcagacc  | tctgaagaga  | gtgccattga  | gacgggttcc  | 3300 |
| 240 | agcagttcca  | ccttcattcaa | gagagaggac  | gagaccattg  | aagacatcga  | catgatggac  | 3360 |
| 241 | gacatcgcca  | tagactcttc  | agacctgggtg | gaagacagct  | tcctgtaact  | ggcggattcg  | 3420 |
| 242 | aggggttcc   | tccacttctg  | gggccacctc  | tggatcccg   | tcagaaaacc  | actttattgc  | 3480 |
| 243 | aatgcggagg  | ttgagaggag  | gacttgggtg  | atgtttaaag  | agaagttccc  | agccaagggc  | 3540 |
| 244 | ctcggggagc  | gttctaaata  | tgaatgaatg  | ggatattttg  | aaatgaactt  | tgtcagtgtt  | 3600 |
| 245 | gcctctcgca  | atgcctcagt  | agcatctcag  | tgggtgtgtg  | agtttggaga  | tagatggata  | 3660 |
| 246 | aggggaataat | aggccacaga  | aggtgaactt  | tgtgcttcaa  | ggacattggg  | gagagtccaa  | 3720 |
| 247 | cagacacaat  | ttatactgcg  | acagaacttc  | agcattgtaa  | ttatgtaaat  | aactctaacc  | 3780 |
| 248 | aaggctgtgt  | ttagattgta  | ttaactatct  | tctttggact  | tctgaagaga  | ccactcaatc  | 3840 |
| 249 | catccatgta  | cttccctctt  | gaaacctgat  | gtcagctgct  | gttgaacttt  | ttaaagaagt  | 3900 |
| 250 | gcatgaaaaa  | ccattttttga | accttaaaaag | gtactggtac  | tatagcattt  | tgctatcttt  | 3960 |
| 251 | tttagtggtta | aagagataaa  | gaataataat  | taaccaacct  | tgtttaatag  | atttgggtca  | 4020 |
| 252 | tttagaagcc  | tgacaactca  | ttttcatatt  | gtaatctatg  | tttataatac  | tactactgtt  | 4080 |
| 253 | atcagtaatg  | ctaaatgtgt  | aataatgtaa  | catgatattcc | ctccagagaa  | agcacaattt  | 4140 |
| 254 | aaaacaatcc  | ttactaagta  | ggtgatgagt  | ttgacagttt  | ttgacattta  | tattaaataa  | 4200 |
| 255 | catgtttctc  | tataaagtat  | ggtaatagct  | ttagtgaatt  | aaatttagtt  | gagcatagag  | 4260 |
| 256 | aacaaagtaa  | aagtagtggt  | gtccaggaag  | tcagaatttt  | taactgtact  | gaatagggtc  | 4320 |

**VERIFICATION SUMMARY**

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